Author index

Abe, T *see* Takasuga, A
Achmann, R *see* Wallner, B
Allendorf, F W *see* Nichols, K M
Alves, E, Óvilo, C, Rodríguez, M C & Silió, L. Mitochondrial DNA sequence variation and phylogenetic relationships among Iberian pigs and other domestic and wild pig populations, 319
Alexander, L J *see* Mickelson, J R.
see also Swinburne, J E
Amano, T *see* Kikkawa, Y
Amills, M & Bouzat, J L. Characterization of the bovine *BCL2L1* gene and related pseudogenes, 457.
Amills, M *see* Tomàs, A
Andelfinger, G, Etter, L, Dyment, M, Hitte, C, Galibert, F, Kirkness, E & Benson, D W. Radiation hybrid mapping and genomic organization of canine *TBX2* and *TBX4*, 307
Anderson, I *see* Guérin, G
Andersson, L *see* Kerje, S.
Antczak, D F *see* Guérin, G
Anthony, N B *see* Cisar, C R
Arthur, J A *see* Kaiser, M G
Åsheim, H-C *see* Bonsdorff, T
Atwell, R B *see* O'Leary, C A
Awata, T *see* Fujishima-Kanaya, F
see also Tanaka, M

Bailey, E *see* Guérin, G
Bailey, J F *see* Edwards, C J
Balmysheva, N *see* Cronin, M A
Balog, J M *see* Cisar, C R
Balzari, M *see* Brenig, B
Barragán, C *see* Toro, M A
Bartenschlager, H *see* Knoll, A.
see also Stratil, A.
see also Wagenknecht, D
Becker, K, Murua Escobar, H, Richter, A, Meyer, B, Nolte, I & Bullerdiek, J. The canine HMGA1 gene maps to CFA 23, 68
Bell, K *see* Guérin, G
Bellmann, O *see* Thaller, G
Bendixen, C *see* Nissen, P H.
see also Harboe, T L
Bennett, G L *see* Connor, E E, Sugimoto, M.
see also Ihara, N
Benson, D W *see* Andelfinger, G
Bentley, J *see* Burt, D W
Bentzen, P *see* Nichols, K M
Bernoco, D *see* Guérin, G
Berryere, T G, Schmutz, S M, Schimpf, R J, Cowan, C M & Potter, J. *TYRP1* is associated with dun coat colour in Dexter cattle or how now brown cow?, 169
Berryere, T G *see* Schmutz, S M
Bertani, G R, Johnson, R K, Robic, A & Pomp, D. Mapping of porcine ESTs obtained from the anterior pituitary, 132
Bigi, D *see* Davoli, R
Binns, M M *see* Mickelson, J R.
see also Swinburne, J E
Biros, I *see* Guérin, G
Bishop, M D *see* Buitkamp, J
Bjornstad, G, Nilsen, N & Roed, K H. Genetic relationship between Mongolian and Norwegian horses?, 55
Bjørnstad, G *see* Guérin, G
Bonsdorff, T, Eggen, A, Gautier, M, Åsheim, H-C, Rønningen, K, Lingaas, F & Olsaker, I. Identification and physical mapping of genes expressed in the *corpus luteum* in cattle, 325
Booij, M *see* te Pas, M F W
Bouzat, J L *see* Amills, M
Bovenhuis, H *see* Siwek, M
Bowling, A T *see* Guérin, G
Bradley, D G *see* Edwards, C J
Braglia, S *see* Davoli, R
Brandon, R *see* Guérin, G
Brem, G *see* Wallner, B
Brenig, B, Pfeiffer, I, Jaggy, A, Kathmann, I, Balzari, M, Gaillard, C & Dolf, G. Analysis of the 5′ region of the canine *PAX3* gene and exclusion as a candidate for Dalmatian deafness, 47.
see also Ren, J.
see also Sena, L
Brown, K H *see* Nichols, K M
Brunelli, J *see* Nichols, K M
Buchanan, F C *see* Thue, T D.
see also Thue, T D
Buitenhuis, A J *see* Siwek, M
Buitkamp, J, Ewald, D, Masabanda, J, Bishop, M D & Fries, R. FISH and RH mapping of the bovine alpha (2)/delta calcium channel subunit gene (*CACNA2D1*), 309
Bullerdiek, J *see* Becker, K
Burt, D W, Morrice, D R, Sewalem, A, Smith, J, Paton, I R, Smith, E J, Bentley, J & Hocking, P M. Preliminary linkage map of the Turkey (*Meleagris gallopavo*) based on microsatellite markers, 399
Burt, D W *see* Paton, I R
Buttazzoni, L *see* Davoli, R

Caetano, A R *see* Guérin, G
Cagnazzo, M *see* Davoli, R
Calvo, J H *see* Roy, R
Carlborg, Ö *see* Kerje, S
Čepica, S & Rohrer, G A. Linkage and radiation hybrid mapping of the porcine *PIK3R1* gene to chromosome 16, 313
Čepica, S *see* Vykoukalová, Z
Chen, L *see* He, C
Cheng, H H *see* Liu, H-C
Cholewinski, G *see* Guérin, G
Christenson, R K *see* Kim, J G.
Cisar, C R, Balog, J M, Okimoto, R, Anthony, N B & Donoghue, A M. The chicken *bone morphogenetic protein receptor type II* gene maps to chromosome 7, 476
Clop, A *see* Tomàs, A
Cnaani, A, Lee, B-Y, Ron, M, Hulata, G, Kocher, T D & Seroussi, E. Linkage mapping of major histocompatibility complex class I loci in tilapia (*Oreochromis* spp.), 390
Colling, D *see* Guérin, G
Comincini, S *see* Hills, D
Connellan, J *see* Edwards, C J
Connor, E E, Sonstegard, T S, Kahl, S, Bennett, G L & Snelling, W M. The bovine type I iodothyronine deiodinase (*DIO1*) gene maps to chromosome 3, 233
Cornelissen, S J B *see* Siwek, M
Cornett, L E *see* Scarbrough, K
Cowan, C M *see* Berryere, T G
Cox, B *see* Lee, M- K
Cronin, M A, Patton, J C, Balmysheva, N & MacNeil, M D. Genetic variation in caribou and reindeer (*Rangifer tarandus*), 33
Crooijmans, R P M A *see* Jungerius, B J, Siwek, M
Cunningham, B M *see* Nichols, K M

Danzmann, R G *see* Nichols, K M.
see also Palti, Y
Davoli, R, Fontanesi, L, Braglia, S & Russo, V. The porcine fast skeletal muscle troponin T3 (*TNNT3*) gene: identification of mutations and linkage mapping to chromosome 2, 391
Davoli, R, Fontanesi, L, Cagnazzo, M, Scotti, E, Buttazzoni, L, Yerle, M & Russo, V. Identification of SNPs, mapping and analysis of allele frequencies in two candidate genes for meat production traits: the porcine myosin heavy chain 2B (*MYH4*) and the skeletal muscle myosin regulatory light chain 2 (*HUMMLC2B*), 221
Davoli, R, Zambonelli, P, Fontanesi, L, Cagnazzo, M, Bigi, D, Russo, V & Milan, D. Radiation hybrid mapping of three skeletal muscle genes (*CKM*, *ECH1* and *TNNT1*) to porcine chromosome 6, 302

© 2003 International Society for Animal Genetics

Davoli, R *see* Stratil, A
Day, A E, Quilter, C R, Sargent, C A & Mileham, A J, Chromosomal mapping, sequence and transcription analysis of the porcine fertilin beta gene (*ADAM2*), 375
Decker, K S *see* Kim, H
Deeb, N & Lamont, S J, Use of a novel outbred by inbred F_1 cross to detect genetic markers for growth, 205
DeSilva, U *see* Guo, X
Di Meo, G P, Perucatti, A, Gautier, M, Hayes, H, Incarnato, D, Eggen, A & Iannuzzi, L, Chromosome localization of the 31 type I Texas bovine markers in sheep and goat chromosomes by comparative FISH-mapping and R-banding, 294
Dodgson, J B *see* Lee, M- K
Dolf, G *see* Brenig, B,
see also Hills, D,
see also Parra, D
Domukai, M *see* Tanaka, M
Donoghue, A M *see* Cisar, C R
Drew, R *see* Nichols, K M
Dunner, S *see* Parra, D
Dvořák, J *see* Vykoukalová, Z
Dyment, M *see* Andelfinger, G

Echternkamp, S E *see* Potts, J K
Eckert, J *see* Geldermann, H
Edwards, C J, Connellan, J, Wallace, P F, Park, S D E, McCormick, F M, Olsaker, I, Eythórsdóttir, E, MacHugh, D E, Bailey, J F & Bradley, D G, Feasibility and utility of microsatellite markers in archaeological cattle remains from a Viking Age settlement in Dublin, 410
Eggen, A *see* Bønsdorff, T,
see also Di Meo, G P,
see also Roy, R
Eggleston, M *see* Guérin, G
Ellis, N *see* Guérin, G
Emara, M G *see* Kim, H
Erhardt, G *see* Weimann, C
Escobar, H M *see* Becker, K
Estellé, J *see* Tomàs, A
Etter, L *see* Andelfinger, G
Ewald, D *see* Buitkamp, J
Ewald, G *see* Thaller, G
Eythórsdóttir, E *see* Edwards, C J

Fan, B, Yang, S-L, Liu, B, Yu, M, Zhao, S-H & Li, K, Characterization of the genetic diversity on natural populations of Chinese miniature pig breeds, 465
Fan, B *see* Wang, Y F,
see also Yu, M
Farber, C R & Medrano, J F, Putative *in silico* mapping of DNA sequences to livestock genome maps using SSLP flanking sequences, 11
Fernández, A, Silió, L, Noguera, J L, Sánchez, A & Óvilo, C, Linkage mapping of the porcine *hairless* gene (*HR*) to chromosome 14, 317
Ferretti, L *see* Hills, D
Fitch, G Q *see* Guo, X
Flynn, J *see* Guérin, G
Folch, J M *see* Yahyaoui, M H
Fontanesi, L *see* Davoli, R,
see also Stratil, A
Forrest, R H, Hickford, J G H, Hogan, A & Frampton, C, Polymorphism at the ovine β_3-adrenergic receptor locus: associations with birth weight, growth rate, carcass composition and cold survival, 19
Frampton, C *see* Forrest, R H
Fredholm, M *see* Proschowsky, H F
Fries, R *see* Buitkamp, J,
see also Ren, J,
see also Thaller, G
Fujishima-Kanaya, N, Toki, D, Suzuki, K, Sawazaki, T, Hiraiwa, H, Iida, M, Hayashi, T, Uenishi, H, Wada, Y, Ito, Y & Awata, T, Development of 50 gene-associated microsatellite markers using BAC clones and the construction of a linkage map of swine chromosome 4, 135
Furuoka, H *see* Sugimoto, M

Gaillard, C *see* Brenig, B
Galibert, F *see* Andelfinger, G
Gauly, M *see* Weimann, C
Gautier, M *see* Bonsdorff, T,
see also Di Meo, G P
Geldermann, H, Preuss, S, Eckert, J, Han, Y & Ollesch, K, Analysis of polymorphic microsatellites within the bovine and ovine prion protein (*PRNP*) genes, 283
Geldermann, H *see* Knoll, A,
see also Stratil, A,
see also Wagenknecht, D
Gilles, M *see* Mamo, S
Gómez-Raya, L *see* Tomàs, A
Goodall, J J & Schmutz, S M, Linkage mapping of *IGF2* on cattle chromosome 29, 313
Goto, R M *see* Iglesias, G M
Gralak, B *see* Guérin, G
Griffin, D K *see* Quilter, C R
Groenen, M A M *see* Jungerius, B J, Siwek, M
Guérin, G, Bailey, E, Bernoco, D, Anderson, I, Antczak, D F, Bell, K, Biros, I, Bjørnstad, G, Bowling, A T, Brandon, R, Caetano, A R, Cholewinski, G, Colling, D, Eggleston, M, Ellis, N, Flynn, J, Gralak, B, Hasegawa, T, Ketchum, M, Lindgren, G, Lyons, L A, Millon, L V, Mariat, D, Murray, J, Neau, A, Roed, K, Sandberg, K, Skow, L C, Tammen, I, Tozaki, T, Van Dyk, E, Weiss, B, Young, A & Ziegle, J, The second generation of the International Equine Gene Mapping Workshop half-sibling linkage map, 161
Guimaraes, S E F *see* Pita, R H, Pita, R H
Guo, X, Kupfer, D M, Fitch, G Q, Roe, B A & DeSilva, U, Identification of a novel lysine-171 allele in the ovine prion protein (*PRNP*) gene, 303

Habermann, F *see* Ren, J
Haegeman, A, Williams, J L, Law, A, Van Zeveren, A & Peelman, L J, Characterization and mapping of bovine dopamine receptors 1 and 5, 290
Haegeman, A, Williams, J L, Law, A, Van Zeveren, A & Peelman, L J, Mapping and SNP analysis of bovine candidate genes for meat and carcass quality, 349
Hagger, C *see* Omi, T
Hamasima, N, Suzuki, H, Mikawa, A, Morozumi, T, Plastow, G & Mitsuhashi, T, Construction of a new porcine whole-genome framework map using a radiation hybrid panel, 216
Han, Y *see* Geldermann, H
Hanotte, O *see* Mburu, D N
Hansen, C *see* Harboe, T L
Harboe, T L, Jensen, L R, Hansen, C, Horn, P, Bendixen, C, Tommerup, N & Tümer, Z, Cloning, characterization and chromosomal localization of the *Sus scrofa SLC31A1* gene, 59
Hartmann, C *see* Kerje, S
Harvey, S C, Kwon, J Y & Penman, D J, Physical mapping of the brain and ovarian aromatase genes in the Nile Tilapia, *Oreochromis niloticus*, by fluorescence in situ hybridization, 62
Hasegawa, T *see* Guérin, G
Hayashi, T *see* Fujishima-Kanaya, F,
see also Tanaka, M
Hayes, H *see* Di Meo, G P,
see also Roy, R
He, C, Chen, L, Simmons, M, Li, P, Kim, S & Liu, Z J, Putative SNP discovery in interspecific hybrids of catfish by comparative EST analysis, 445
Hickford, J G H *see* Forrest, R H
Hills, D, Schlaepfer, J, Comincini, S, MacLean, I, Dolf, G, Ferretti, L, Olsaker, I & Williams, J L, Sequence variation in the bovine and ovine *PRNP* genes, 183
Hiraiwa, H *see* Fujishima-Kanaya, F
Hitte, C *see* Andelfinger, G
Hocking, P M *see* Burt, D W
Hogan, A *see* Forrest, R H
Honeycutt, R L *see* Sena, L
Horn, P *see* Harboe, T L
Hu, X *see* Wang, A, Wang, A
Huang, L S *see* Ren, J
Hughes, C R *see* Stai, S M
Hulata, G *see* Cnaani, A

Iannuzzi, L *see* Di Meo, G P
Iglesias, G M, Soria, L A, Goto, R M, Jar, A M, Miquel, M C, Lopez, O J & Miller, M M. Genotypic variability at the major histocompatibility complex (*B and Rfp-Y*) in Camperos broiler chickens. 88
Ihara, N, Yamakuchi, H, Taniguchi, Y, Sasaki, Y, Bennett, G L, Kappes, S & Sugimoto, Y. Mapping of bovine *CEBPD* gene to BTA14q15–17. 470
Ihara, N *see* Sugimoto, M
Iida, M *see* Fujishima-Kanaya, F
Incarnato, D *see* Di Meo, G P
Itoh, T, Takasuga, A, Watanabe, T & Sugimoto, Y. Mapping of 1400 expressed sequence tags in the bovine genome using a somatic cell hybrid panel. 362
Ito, T *see* Takasuga, A,
see also Fujishima-Kanaya, F

Jacobsson, L *see* Kerje, S
Jaggy, A *see* Brenig, B
Jar, A M *see* Iglesias, G M
Jensen, L R *see* Harboe, T L
Jensen, P *see* Kerje, S,
see also Kerje, S
Jepsen, B *see* Proschowsky, H F
Jianlin, H *see* Mburu, D N
Johnson, R K *see* Bertani, G R
Jungerius, B J, Rattink, A P, A Crooijmans, R P M, van der Poel, J J, van Oost, B A, te Pas, M F W & Groenen, M A M. Development of a single nucleotide polymorphism map of porcine chromosome 2. 429

Kahl, S *see* Connor, E E
Kaiser, M G, Lakshmanan, N, Arthur, J A, O'Sullivan, N P & Lamont, S J. Experimental population design for estimation of dominant molecular marker effect on egg-production traits. 334
Kajii, E *see* Omi, T
Kamatani, N *see* Takasuga, A
Kappes, S *see* Ihara, N
Kata, S R *see* Mamo, S
Kathmann, I *see* Brenig, B
Kaufmann, B *see* Mburu, D N
Kerje, S, Carlborg, Ö, Jacobsson, L, Schütz, K, Hartmann, C, Jensen, P & Andersson, L. The twofold difference in adult size between the red junglefowl and White Leghorn chickens is largely explained by a limited number of QTLs. 264
Kerje, S, Lind, J, Schütz, K, Jensen, P & Andersson, L. Melanocortin 1-receptor (*MC1R*) mutations are associated with plumage colour in chicken. 241
Ketchum, M *see* Guérin, G
Khoo, S-K *see* Ozaki, A
Kikkawa, Y, Takada, T, Sutopo, Nomura, K, Namikawa, T, Yonekawa, H & Amano, T. Phylogenies using mtDNA and *SRY* provide evidence for male-mediated introgression in Asian domestic cattle. 96
Kim, H, Schmidt, C J, Decker, K S & Emara, M G. A double-screening method to identify reliable candidate non-synonymous SNPs from chicken EST data. 249
Kim, J G, Nonneman, D, Rohrer, G A, Vallet, J L & Christenson, R K. Linkage mapping of a SNP in the porcine *MADH1* gene to a region of chromosome 8 that contains QTL for uterine capacity. 310
Kim, J G, Nonneman, D, Vallet, J L & Christenson, R K. Linkage mapping of the porcine testis enhanced gene transcript (*TEGT*) gene to chromosome 5. 152
Kim, J G, Smith, T P L, Snelling, W M, Vallet, J L & Christenson, R K. Linkage mapping of the bovine bone morphogenetic protein receptor- 1B (*BMPR1B*) to chromosome 6. 311
Kim, S *see* He, C
Kirby, J D *see* Scarbrough, K
Kirkness, E *see* Andelfinger, G,
see also Kothapalli, K S D
Kirkpatrick, B W *see* Kurar, E
Kiuchi, S *see* Tanaka, M
Knol, E F *see* te Pas, M F W
Knoll, A, Stratil, A, Vykoukalová, Z, Van Poucke, M, Bartenschlager, H, Peelman, L J & Geldermann, H. Polymorphism analysis and mapping to SSC4 of the porcine apolipoprotein A2 (*APOA2*) gene. 384
Knoll, A *see* Vykoukalová, Z
Knorr, C *see* Ren, J
Knudsen, K *see* Nichols, K M
Kobayashi, E *see* Tanaka, M
Kocher, T D *see* Cnaani, A, Lee, B-Y
Koskinen, M T. Individual assignment using microsatellite DNA reveals unambiguous breed identification in the domestic dog. 297
Kothapalli, K S D, Kirkness, E, Natale, L J & Meyers-Wallen, V N. Exclusion of *PISRT1* as a candidate locus for canine *Sry*-negative XX sex reversal. 468
Kramer, J, Malek, M & Lamont, S J. Association of twelve candidate gene polymorphisms and response to challenge with *Salmonella enteritidis* in poultry. 339
Kramer, J *see* Stratil, A
Kraus, M *see* Weimann, C
Kühn, C *see* Thaller, G
Kupfer, D M *see* Guo, X
Kurar, E, Womack, J E & Kirkpatrick, B W. A radiation hybrid map of bovine chromosome 24 and comparative mapping with human chromosome 18. 198
Kuria, S G *see* Mburu, D N
Kwon, J Y *see* Harvey, S C

Lagonigro, R, Wiener, P, Pilla, F, Woolliams, J A & Williams, J L. A new mutation in the coding region of the bovine leptin gene associated with feed intake. 371
Laing, N G *see* O'Leary, C A
Lakshmanan, N *see* Kaiser, M G
Lamont, S J *see* Deeb, N,
see also Kaiser, M G,
see also Kramer, J,
see also Zhou, H
Law, A *see* Haegeman, A
Lee, B-Y, Penman, D J & Kocher, T D. Identification of a sex-determining region in Nile tilapia (*Oreochromis niloticus*) using bulked segregant analysis. 379
Lee, B-Y *see* Cnaani, A
Lee, M-K, Ren, C W, Yan, B, Cox, B, Zhang, H- B, Romanov, M N, Sizemore, F G, Suchyta, S P, Peters, E & Dodgson, J B. Construction and characterization of three BAC libraries for analysis of the chicken genome. 151
Leenhouwers, J I *see* te Pas, M F W
van der Lende, T *see* te Pas, M F W
Li, K *see* Fan, B,
see also Pan, P-W,
see also Wang, Y F
Li, N *see* Wang, A,
Li, P *see* He, C
Lind, J *see* Kerje, S
Lindgren, G *see* Guérin, G
Lingaas, F *see* Bonsdorff, T
Liu, B *see* Fan, B,
see also Pan, P-W,
see also Wang, Y F,
see also Yu, M,
Liu, H-C & Cheng, H H. Genetic mapping of the chicken stem cell antigen 2 (SCA2) gene to chromosome 2 via PCR primer mutagenesis. 158
Liu, Z J *see* He, C
Long, J-R, Qiu, X-P, Zeng, F-T, Tang, L-M & Zhang, Y-P. Origin of rabbit (*Oryctolagus cuniculus*) in China: evidence from mitochondrial DNA control region sequence analysis. 82
Lopes, P S *see* Pita, R H, Pita, R H
Lopez, O J *see* Iglesias, G M
Lyons, L A *see* Guérin, G

MacHugh, D E *see* Edwards, C J
MacLean, I *see* Hills, D
MacNeil, M D *see* Cronin, M A
Majzlik, I *see* Wagenknecht, D
Malek, M *see* Kramer, J
Mallard, B A *see* Sharif, S

Mamo, S. Wimmers, K. Gilles, M. Kata, S R. Schellander, K & Ponsuksili, S. Mapping of ESTs derived from pre-implantation stage cattle embryos to allocate 16 new additions to the ordered comparative map of cattle and human, 449
Mannen, H *see* Sultana, S
Mariat, D *see* Guérin, G
Masabanda, J *see* Buitkamp, J
Matsumoto, T *see* Tanaka, M
Mau, C. Stranzinger, G & Rieder, S. Polymorphisms in the equine *WNT1* gene allow linkage mapping to ECA6q, 148
Mburu, D N, Ochieng, J W, Kuria, S G, Jianlin, H, Kaufmann, B, Rege, J E O & Hanotte, O. Genetic diversity and relationships of indigenous Kenyan camel (*Camelus dromedarius*) populations: implications for their classification, 26
McCormick, F M *see* Edwards, C J
McDaneld, T G & Moody, D E. Characterization of a bovine gene encoding an ankyrin repeat and SOCS box protein (*ASB15*), 235
Medrano, J F *see* Farber, C R
Meyer, B *see* Becker, K
Meyers-Wallen, V N *see* Kothapalli, K S D
Michalak, E *see* Szczerbal, I
Mickelson, J R, Wu, J T, Morrison, L Y, Swinburne, J E, Binns, M M, Reed, K M & Alexander, L J, Eighty-three previously unreported equine microsatellite loci, 71
Mickleson, J R *see* Swinburne, J E
Mikawa, A *see* Hamasima, N
Milan, D *see* Davoli, R
Mileham, A J *see* Day, A E
Miller, M M *see* Iglesias, G M
Millon, L V *see* Guérin, G
Miquel, M C *see* Iglesias, G M
Mishra, B P & Reecy, J M. Mutations in the *limbin* gene previously associated with dwarfism in Japanese brown cattle are not responsible for dwarfism in the American Angus breed, 311
Mitsuhashi, T *see* Hamasima, N
Moody, D E *see* McDaneld, T G
Morozumi, T *see* Hamasima, N
Morrice, D R *see* Burt, D W
Morrison, L Y *see* Mickelson, J R
Müller, M *see* Wallner, B
Muñoz, G, Óvilo, C, Noguera, J L, Sánchez, A, Rodríguez, C & Silió, L. Assignment of the fatty acid synthase (FASN) gene to pig chromosome 12 by physical and linkage mapping, 234
Murray, J *see* Guérin, G
Murua Escobar, H *see* Becker, K
Namikawa, T *see* Kikkawa, Y
Natale, L J *see* Kothapalli, K S D
Neau, A *see* Guérin, G
Neuenschwander, S *see* Omi, T
Nichols, K M, Young, W P, Danzmann, R G, Robison, B D, Rexroad, C, Noakes, M, Phillips, R B, Bentzen, P, Spies, I, Knudsen, K, Allendorf, F W, Cunningham, B M, Brunelli, J, Zhang, H, Ristow, S, Drew, R, Brown, K H, Wheeler, P A & Thorgaard, G H. A consolidated linkage map for rainbow trout (*Oncorhynchus mykiss*), 102
Nieuwland, M G B *see* Siwek, M
Nilsen, N *see* Bjornstad, G
Nissen, P H, Thomsen, B, Offenberg, H, Thomsen, P D & Bendixen, C. Cloning and characterization of the bovine *EGR4* gene and evaluation as candidate gene for bovine spinal dysmyelination, 124
Noakes, M A & Phillips, R B. OtY1 is a Y-linked marker in Chinook salmon but not in Rainbow trout, 156
Noakes, M *see* Nichols, K M
Noguera, J L *see* Fernández, A.
see also Muñoz, G.
see also Tomás, A
Nolte, I *see* Becker, K
Nomura, K *see* Kikkawa, Y
Nonneman, D & Rohrer, G A. Molecular cloning of the porcine *inhibin*-βB gene and reassignment to chromosome 15, 213
Nonneman, D *see* Kim, J G
Nonneman, D J & Rohrer, G A. Comparative mapping of a region on chromosome 10 containing QTL for reproduction in swine, 42

Ochieng, J W *see* Mburu, D N
Offenberg, H *see* Nissen, P H
Okamoto, N *see* Ozaki, A
Okimoto, R *see* Cisar, C R.
see also Scarbrough, K
O'Leary, C A, Atwell, R B & Laing, N G. No disease-associated mutations found in the coding sequence of the canine polycystic kidney disease gene 1 in Bull Terriers with polycystic kidney disease, 358
Ollesch, K *see* Geldermann, H
Olsaker, I *see* Bonsdorff, T.
see also Edwards, C J.
see also Hills, D
Olsen, J B *see* Proschowsky, H F
Omi, T, Vögeli, P, Hagger, C, Schelling, C, Špilar, Š, Kajii, E, Stranzinger, G & Neuenschwander, S. cDNA cloning, mapping and polymorphism of the porcine *Rhesus* (*RH*) gene, 176
van Oost, B A *see* Jungerius, B J
O'Sullivan, N P *see* Kaiser, M G
Óvilo, C *see* Alves, E.
see also Fernández, A.
see also Muñoz, G.
see also Toro, M A
Ozaki, A, Khoo, S-K, Sakamoto, T & Okamoto, N. Thirty-one polymorphic microsatellite markers for genetic mapping in rainbow trout (*Oncorhynchus mykiss*), 315

Palti, Y, Danzmann, R G & Rexroad, C E III. Characterization and mapping of 19 polymorphic microsatellite markers for rainbow trout (*Oncorhynchus mykiss*), 153
Pan, P *see* Yu, M
Pan, P-W, Li, K, Tuggle, C K, Yu, M, Liu, B & Zhao, S-H. Sequencing, tissue distribution and physical mapping of the porcine homologue of cardiomyopathy associated 3 (*CMYA3*), 472
Park, S D E *see* Edwards, C J
Parra, D, Dolf, G & Dunner, S. Contribution of a new set of canine microsatellites to the knowledge of the canine genetic map, 69
Parmentier, H K *see* Siwek, M
te Pas, M F W, Leenhouwers, J I, Knol, E F, Booij, M, Priem, J & van der Lende, T. Marker polymorphisms in the porcine genes for muscle glycogen synthase (GYS1) and muscle glycogen phosphorylase (PYGM), 157
te Pas, M F W *see* Jungerius, B J
Paton, I R, Smith, J & Burt, D W. Chicken syndecan-4 (*SDC4*) maps to linkage group E32E47W24, 237
Paton, I R, Smith, J & Burt, D W. Mapping the *ABCA4*, *IMPDH2* and *TIMP3* genes in chicken, 395
Paton, I R *see* Burt, D W
Patton, J C *see* Cronin, M A
Peelman, L J *see* Haegeman, A.
see also Knoll, A.
see also Haegeman, A.
see also Stratil, A.
see also Wagenknecht, D
Penman, D J *see* Lee, B-Y.
see also Harvey, S C
Perucatti, A *see* Di Meo, G P
Peters, E *see* Lee, M- K
Pfeiffer, I *see* Brenig, B
Phillips, R B *see* Nichols, K M.
see also Noakes, M A
Pilla, F *see* Lagonigro, R
Pita, R H, Ramos, A M, Lopes, P S, Guimaraes, S E F & Rothschild, M F. Assignment of the *porcine peptide YY* gene to chromosome 12, 469
Pita, R H, Ramos, A M, Lopes, P S, Guimaraes, S E F & Rothschild, M F. Mapping of the porcine *peroxisome proliferator activated receptor alpha* gene to chromosome 5, 469
Plastow, G *see* Hamasima, N,
van der Poel, J J *see* Siwek, M.
see also Jungerius, B J
Poli, M, Sala, L & Zandomeni, R. Identification of a new BoLA-*DRB*3.2 allele, 389

Pomp, D *see* Bertani, G R
Ponsuksili, S *see* Mamo, S
Potter, J *see* Berryere, T G
Potts, J K, Echternkamp, S E, Smith, T P L & Reecy, J M. Characterization of gene expression in double-muscled and normal-muscled bovine embryos, 438
Preuss, S *see* Geldermann, H
Priem, J *see* te Pas, M F W
Proschowsky, H F, Olsen, J B, Jepsen, B & Fredholm, M. Evaluation of the present breeding programme against copper toxicosis in Danish Bedlington terriers, 142

Qiu, X-P *see* Long, J-R
Quilter, C R, Wood, D, Southwood, O I & Griffin, D K. X/XY/XYY mosaicism as a cause of subfertility in boars: a single case study, 51
Quilter, C R *see* Day, A E

Ramos, A M *see* Pita, R H, Pita, R H
Rattink, A P *see* Jungerius, B J
Reecy, J M *see* Mishra, B P,
see also Potts, J K
Reed, K M *see* Mickelson, J R
Rege, J E O *see* Mburu, D N
Ren, C W *see* Lee, M- K
Ren, J, Knorr, C, Habermann, F, Fries, R, Huang, L S & Brenig, B. Assignment of the porcine stearoyl-CoA desaturase (*SCD*) gene to SSC14q27 by fluorescence *in situ* hybridization and by hybrid panel mapping, 471
Rexroad, C *see* Nichols, K M
Rexroad, C E III *see* Palti, Y
Rieder, S *see* Mau, C
Richter, A *see* Becker, K
Ristow, S *see* Nichols, K M
Robic, A *see* Bertani, G R
Robison, B D *see* Nichols, K M
Rodellar, C *see* Roy, R
Rodríguez, C *see* Muñoz, G
Rodríguez, M C *see* Alves, E
Roe, B A *see* Guo, X
Roed, K *see* Guérin, G
Roed, K H *see* Bjørnstad, G
Rohrer, G A *see* Čepica, S,
see also Kim, J G,
see also Nonneman, D J,
see also Nonneman, D,
see also Vykoukalová, Z
Romanov, M N *see* Lee, M- K
Ron, M *see* Cnaani, A
Ronningen, K *see* Bonsdorff, T
Rothschild, M F *see* Pita, R H, Pita, R H
Roy, R, Calvo, J H, Hayes, H, Rodellar, C & Eggen, A. Fine mapping of the bovine heart fatty acid-binding protein gene (*FABP3*) to BTA2q45 by fluorescence *in situ* hybridization and radiation hybrid mapping, 466
Russo, V *see* Davoli, R
see also Stratil, A

Sakamoto, T *see* Ozaki, A
Sala, L *see* Poli, M
Sánchez, A *see* Fernández, A,
see also Muñoz, G,
see also Tomàs, A,
see also Yahyaoui, M H
Sandberg, K *see* Guérin, G
Sargent, C A *see* Day, A E
Sasaki, Y *see* Ihara, N
Sawazaki, T *see* Fujishima-Kanaya, N
Scarbrough, K, Kirby, J D, Cornett, L E & Okimoto, R. Chromosomal assignment and mapping of the Vasotocin Receptor 1, homologue to the mammalian V1a and Vasotocin Receptor 2 homologue to the mammalian V1b receptors in the domestic fowl, 393
Schellander, K *see* Mamo, S
Schelling, C *see* Omi, T
Schimpf, R J *see* Berryere, T G
Schlaepfer, J *see* Hills, D
Schmidt, C J *see* Kim, H
Schmutz, S M, Berryere, T G & Sharp, C A. *KITLG* maps to canine chromosome 15 and is excluded as a candidate gene for merle in dogs, 75
Schmutz, S M *see* Berryere, T G,
see also Goodall, J J
Schneider, M P C *see* Sena, L
Schütz, K *see* Kerje, S,
see also Kerje, S
Scotti, E *see* Davoli, R,
see also Stratil, A
Sena, L, Schneider, M P C, Brenig, B, Honeycutt, R L, Womack, J E & Skow, L C. Polymorphisms in MHC-*DRA* and -*DRB* alleles of water buffalo (*Bubalus bubalis*) reveal different features from cattle *DR* alleles, 1
Seroussi, E *see* Cnaani, A
Sewalem, A *see* Burt, D W
Sharif, S, Mallard, B A & Wilkie, B N. Characterization of naturally processed and presented peptides associated with bovine major histocompatibility complex (BoLA) class II DR molecules, 116
Sharp, C A *see* Schmutz, S M
Silió, L *see* Alves, E,
see also Fernández, A,
see also Muñoz, G
Simmons, M *see* He, C
Siraj, S S *see* Usmani, S
Siwek, M, Cornelissen, S J B, Nieuwland, M G B, Buitenhuis, A J, Bovenhuis, H, A Crooijmans, R P M, Groenen, M A M, de Vries-Reilingh, G, Parmentier, H K & van der Poel, J J. Detection of QTL for immune response to sheep red blood cells in laying hens, 422
Sizemore, F G *see* Lee, M- K
Skow, L C *see* Guérin, G,
see also Sena, L
Smith, E J *see* Burt, D W
Smith, J *see* Burt, D W,
see also Paton, I R,
see also Kim, J G
Smith, T P L *see* Potts, J K
Snelling, W M *see* Connor, E E,
see also Kim, J G
Sonstegard, T S *see* Connor, E E
Soria, L A *see* Iglesias, G M
Southwood, O I *see* Quilter, C R
Spies, I *see* Nichols, K M
Špilar, Š *see* Omi, T
Stai, S M & Hughes, C R. Characterization of microsatellite loci in wild and domestic Muscovy ducks (*Cairina moschata*), 387
Stranzinger, G *see* Mau, C
see also Omi, T
Stratil, A, Blažková, P, Kopečný, M, Bartenschlager, H, Van Poucke, M, Peelman, L J, Fontanesi, L, Davoli, R, Scotti, E, Russo, V & Geldermann, H. Characterization of a SINE indel polymorphism in the porcine *AGL* gene and assignment of the gene to chromosome 4q, 146
Stratil, A *see* Knoll, A,
see also Wagenknecht, D
Suchyta, S P *see* Lee, M- K
Sugimoto, M, Furuoka, H & Sugimoto, Y. Deletion of one of the duplicated *Hsp70* genes causes hereditary myopathy of diaphragmatic muscles in Holstein-Friesian cattle, 191
Sugimoto, M, Ihara, N, Bennett, G L & Sugimoto, Y. Eleven previously unreported dinucleotide microsatellite loci on bovine chromosome 19, 236
Sugimoto, Y *see* Ihara, N,
see also Itoh, T,
see also Takasuga, A,
see also Sugimoto, M,
see also Sugimoto, M
Sultana, S, Mannen, H & Tsuji, S. Mitochondrial DNA diversity of Pakistani goats, 417
Suzuki, H *see* Hamasima, N
Suzuki, K *see* Fujishima-Kanaya, N
Swinburne, J E, Turner, A, Alexander, L J, Mickleson, J R & Binns, M M. Characterization and linkage map assignments for 61 new horse microsatellite loci (*AHT49–109*), 65
Swinburne, J E *see* Mickelson, J R
Szczerbal, I & Michalak, E. FISH-localization of the nucleolar organizer region on the feline E1p12 chromosome, 386

Takada, T *see* Kikkawa, Y
Takasuga, A, Abe, T, Ito, T, Watanabe, T, Kamatani, N & Sugimoto, Y. Novel prion protein polymorphisms in cattle, 396

Takasuga, A *see* Itoh, T
Tammen, I *see* Guérin, G
Tan, S G *see* Usmani, S
Tanaka, M, Matsumoto, T, Yanai, S, Domukai, M, Toki, D, Hayashi, T, Kiuchi, S, Yasue, H, Uenishi, H, Kobayashi, E & Awata, T. Conservation of the syntenies between porcine chromosome 7 and human chromosomes 6, 14 and 15 demonstrated by radiation hybrid mapping and linkage analysis, 255
Tang, L-M *see* Long, J-R
Taniguchi, Y *see* Ihara, N
Thaller, G, Kühn, C, Winter, A, Ewald, G, Bellmann, O, Wegner, J, Zühlke, H & Fries, R. *DGAT1*, a new positional and functional candidate gene for intramuscular fat deposition in cattle, 354
Thomsen, B *see* Nissen, P H
Thomsen, P D *see* Nissen, P H
Thorgaard, G H *see* Nichols, K M
Thue, T D & Buchanan, F C. Linkage mapping of *FBN1* to bovine chromosome 10, 150
Thue, T D & Buchanan, F C. Linkage mapping of *POMC* to bovine chromosome 11, 149
Toki, D *see* Fujishima-Kanaya, N
see also Tanaka, M
Tomàs, A, Estellé, J, Clop, A, Gómez-Raya, L, Noguera, J L, Sánchez, A & Amills, M. Assignment of the mitochondrial *glycerol-3-phosphate acyltransferase* (*GPAT*) gene to porcine chromosome 14, 387
Tommerup, N *see* Harboe, T L
Toro, M A, Barragán, C & Óvilo, C. Estimation of genetic variability of the founder population in a conservation scheme using microsatellites, 226
Tozaki, T *see* Guérin, G
Tsuji, S *see* Sultana, S
Tuggle, C K *see* Pan, P-W
Tümer, Z *see* Harboe, T L
Turner, A *see* Swinburne, J E

Uenishi, H *see* Fujishima-Kanaya, N
see also Tanaka, M
Usmani, S, Tan, S G, Siraj, S S & Yusoff, K. Population structure of the Southeast Asian river catfish *Mystus nemurus*, 462

Vaiman, D *see* Yahyaoui, M H
Vallet, J L *see* Kim, J G,
see also Kim, J G,
see also Kim, J G
Van Dyk, E *see* Guérin, G
Van Poucke, M *see* Knoll, A,
see also Stratil, A,
see also Wagenknecht, D
Van Zeveren, A *see* Haegeman, A
Vögeli, P *see* Omi, T
de Vries-Reilingh, G *see* Siwek, M
Vykoukalová, Z, Knoll, A, Dvořák, J, Rohrer, G A & Čepica, S. Linkage and radiation hybrid mapping of the porcine *MYF6* gene to chromosome 5, 238
Vykoukalová, Z *see* Knoll, A

Wada, Y *see* Fujishima-Kanaya, N
Wagenknecht, D, Stratil, A, Bartenschlager, H, Van Poucke, M, Peelman, L J, Majzlík, I & Geldermann, H. Linkage and radiation hybrid mapping of the porcine *MEF2D* gene to chromosome 4q, 232
Wallace, P F *see* Edwards, C J
Wallner, B, Brem, G, Müller, M & Achmann, R. Fixed nucleotide differences on the Y chromosome indicate clear divergence between *Equus przewalskii* and *Equus caballus*, 453
Wang, A, Hu, X, Li, N & Wu, C. *BMPR1B* maps to chromosome 8 in swine, 306
Wang, A, Hu, X, Li, N & Wu, C. Characterization of three single nucleotide polymorphisms in the porcine *BMP15* gene, 305
Wang, Y F, Yu, M, Yerle, M, Liu, B, Zhao, S H, Xiong, T A, Fan, B & Li, K. Mapping of genes encoding four ATPase and three non-ATPase components of the pig 26S proteasome, 393
Watanabe, T *see* Itoh, T,
see also Takasuga, A
Wegner, J *see* Thaller, G
Weimann, C, Kraus, M, Gauly, M & Erhardt, G. Differences in recombination rates on chromosome 23 between German Angus and German Simmental and breed specific linkage mapping, 229
Weiss, B *see* Guérin, G
Wheeler, P A *see* Nichols, K M
Wiener, P *see* Lagonigro, R
Wilkie, B N *see* Sharif, S
Williams, J L *see* Haegeman, A,
see also Lagonigro, R,
see also Hills, D
Wimmers, K *see* Mamo, S
Winter, A *see* Thaller, G
Womack, J E *see* Kurar, E
see also Sena, L
Wood, D *see* Quilter, C R
Woolliams, J A *see* Lagonigro, R
Wu, C *see* Wang, A,
see also Wang, A
Wu, J T *see* Mickelson, J R

Xiong, T A *see* Wang, Y F

Yahyaoui, M H, Vaiman, D, Sánchez, A & Folch, J M. Mapping of the goat *stearoyl coenzyme A desaturase* gene to chromosome 26, 473
Yamakuchi, H *see* Ihara, N
Yan, B *see* Lee, M- K
Yanai, S *see* Tanaka, M
Yang, S-L *see* Fan, B
Yasue, H *see* Tanaka, M
Yerle, M *see* Davoli, R,
see also Wang, Y F,
see also Yu, M,
see also Kikkawa, Y
Young, A *see* Guérin, G
Young, W P *see* Nichols, K M
Yu, M, Liu, B, Yerle, M, Zhu, M, Pan, P, Fan, B & Li, K. Physical mapping of the rod cGMP- phosphodiesterase γ-subunit (*PDE6G*) gene to pig chromosome 12, 76
Yu, M *see* Fan, B,
see also Pan, P-W,
see also Wang, Y F
Yusoff, K *see* Usmani, S

Zambonelli, P *see* Davoli, R
Zandomeni, R *see* Poli, M
Zeng, F-T *see* Long, J-R
Zhang, H- B *see* Lee, M-K,
see also Nichols, K M
Zhang, Y-P *see* Long, J-R
Zhao, S H *see* Wang, Y F,
see also Fan, B,
see also Pan, P-W
Zhou, H & Lamont, S J. Association of transforming growth factor β genes with quantitative trait loci for antibody response kinetics in hens, 275
Zhu, M *see* Yu, M
Ziegle, J *see* Guérin, G
Zühlke, H *see* Thaller, G

Keyword index

abnormal genitalia 51
ADAM2 375
additive effects 264
allele frequency 221
amplified fragment length polymorphism 102
ancient DNA 410
animal genome mapping 11
anterior pituitary 132
antibody response kinetics 275
antigen presentation 116
antigen-binding groove 116
aquaculture 379, 445
aromatase 62
autosomal recessive disease 191
average daily gain 221

β_3-adrenergic receptor 19
BAC 375
BAC library 135
bacterial artificial chromosome 62
Bayesian methods 297
biomolecular archaeology 410
BoLA class II alleles 116
bovine 96, 438
bovine chromosome 24 198
bovine spinal dysmyelination gene 124
breed identification 297
breed relationships 410
broilers 88, 205
brown 169
BSE 183
BTA8 169

candidate gene 124, 339
carcass composition 19
caribou 33
cattle 124, 229, 283, 325, 354, 362
CFA37 47
chicken 88, 241, 249, 264, 334, 422
chromosome 161
chromosome 14 354
chromosome 15 213
chromosome 23 229
cloning 176
coat colour 169
cold 19
comparative map 42, 213, 255, 449
complementary deoxyribonucleic acid 290
control region 82
Copper metabolism 59
copper toxicosis 142
corpus luteum 325
CTR1 59
Cyt B 319
cytochrome *b* 417
cytogenetics 294

Dalmatian 47
deafness 47
deoxyribo nucleic acid pools 205
Dexter 169
DGAT1 354
differentiation index value (F_{ST}) 26
dilution 169
disease association 116
dispersal 55
D-loop 319
D-loop 417
DNA fingerprint 334
DNA markers 283
dog 358
dog breed 142
domestic dog 297
domestication 96
dominant marker system 334
dopamine receptor 290
double-screening 249
DRA 1
DRB 1
dromedary camel 26
dun 169

egg production 264
egg production traits 334
EGR4 124
enriched library 399
Equus caballus 453
Equus przewalskii 453
ESTs 132
European cattle 410
expressed sequence tag 445
expressed sequence tag data mining 249
expressed sequence tags 11, 325, 362, 449
Extended black 241

F_1 205
feed intake 371
fertilin 375
FISH 375
fish 445
fluorescence in situ hybridization 62
founder 226
framework map 216

gene expression 438
gene marker 19
genealogy 226
gene-associated marker 255
genetic admixture 297
genetic diversity 26, 82
genetic introgression 96
genetic resistance 339
genetic variability 88, 462
genetic variation 33, 142
genome 161
goat 294
growth 264

heterozygosity 142
Holstein-Friesian cattle 191
horse 161
horse breed history 55
Hsp70 191

Iberian pig 226
Iberian pigs 319
immune response 422
in silico 11
inbred 205
inbred line 275
individual assignment 26, 297
infertility 51
inhibin-βB 213
intramuscular fat 354

leptin 371
linkage analysis 191, 255
linkage group 161
linkage map 135, 399
linkage mapping 229
livestock production 371

macroarray 438
major histocompatibility complex 88
mapping 132, 161, 176, 449
marbling 354
marker 445
markers 161
mass spectrometry 116
maternal origin 417
MC1R 169, 241
medieval Dublin 410
MHC polymorphism 1
MHC-*Bubu* 1
microsatellite 11, 26, 42, 142, 161, 213, 226, 229, 255, 362, 410, 462
microsatellite DNA 33
microsatellite marker isolation 135
microsatellite markers 399
microsatellites 55, 102, 297
migration 55
Mongolian horse 55
mosaicism 51
mtDNA 82, 96, 319
mutation 290
myopathy 191
myosin heavy chain-2B 221
myosin regulatory light chain 2 221
myostatin 438
Mystus nemurus 462

© 2003 International Society for Animal Genetics

nomenclature 294
non-synonymous 249
Northern European horse breeds 55

obese gene 371
Oncorhynchus mykiss 102
Oreochromis 379
Oreochromis niloticus 62
origin 82
outbred 205
ovary 325
ovine 19

P450 62
paired-box gene 3 47
Pakistani goat 417
peptide-binding motifs 116
phylogenetic analysis 417
phylogeny 453
pig 176, 216, 221, 255, 429
pigmentation 169
plumage colour 241
polycystic kidney disease 358
polycystic kidney disease gene 1 358
polymerase chain reaction 290
polymerase chain reaction–single strand conformational polymorphism 19
polymorphism 19, 183, 462
population differentiation 26
population structure 462
porcine 213, 429
porcine chromosome 10 42
pre-implantation embryo 449
prion 183
prion protein 283
PRNP 283

quantitative trait loci 422
quantitative trait loci detection 334
Quantitative Trait Locus 264

rabbit 82
radiation hybrid map 198
radiation hybrid mapping 255, 349, 449
radiation hybrid panel 216, 325
Rangifer 33
recombination rate 229
regional localization 362
reindeer 33
representational difference analysis 325
resource population 334
restriction fragment length polymorphism 290
RFLP 349
rhesus (*RH*) gene 176

Salmonella enteritidis challenge 339
scrapie 183
segregation 161
selection 422
sequence tagged site 255
sex chromosome abnormalities 51
sex chromosomes 379
sex linkage 379
sheep 283, 294
sheep red blood cells 422
Sindh Ibex 417
single nucleotide polymorphism 275, 339, 445
SLC31A1 59
SNP 42, 183, 249, 349, 371, 429
somatic cell hybrid panel 325, 362
spinal dysmyelination 124
SRY 96
SSC2 429
SSCP 290, 349
step-wise elimination procedure 275
subtractive hybridization 325
survival 19
Sus scrofa 59
swine 132, 135

TG 354
Tilapia 62, 379
transfectants 116
transforming growth factor β genes 275
turkey 399
type I marker 294
type I markers 102
TYRP1 169

VNTR (variable number of tandem repeats) 283

Waardenburg syndrome 47
water buffalo 1
whole-genome 216
wild boars 319

Y chromosome 453